

Modelling the biomass yield and the impact of seabream mariculture in the Adriatic and Tyrrhenian Seas (Italy)

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Abstract An individual-based model for *Sparus aurata* was developed, taking into account the effects on the growth rate of water temperature, food availability and diet composition. The model was identified on the basis of the recent literature regarding the physiological ecology of this species. It was subsequently calibrated and validated by using original field data collected at two Italian fish farms located, respectively, in the Adriatic and Tyrrhenian Seas. The mass budget of uneaten food and faeces was computed using the model at each farm: the optimal ingestion rate of a fish was computed based on its wet weight and the temperature of the water, while the faeces estimation considered the different digestibility of lipids, carbohydrates and proteins in the diet. From an applied perspective, the future use of this growth model in relation to mariculture site selection and monitoring might typically be to estimate both the yield and the amount of uneaten food and faeces discharged from a fish cage. This second output represents a useful input for deposition models which are routinely used in the field of mariculture monitoring by different EU countries. The integration of growth and deposition models in a single system could provide a useful tool for the site-selection and monitoring of finfish mariculture operations in Mediterranean environments.

Keywords Environmental impact assessment · Individual-based model ·
Mariculture impacts · Site selection · *Sparus aurata*

Introduction

Over the last few decades, the production of finfish marine aquaculture in Italy has rapidly increased because of both the increase in the number of sites and in the site-specific

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productivity. The gilthead seabream (*Sparus aurata* L.) and European Seabass (*Dicentrarchus labrax* L.) are the two most important species, representing approximately 90% of the Italian finfish mariculture production in 2005 (FAO 2007).

In order to manage the development of Italian aquaculture in a sustainable way, as required by European legislation, the application of optimisation criteria that allow maximising the yield while minimising the negative environmental impacts is mandatory.

Mathematical models have proved to be useful tools for site selection and for assessing and monitoring the impact of mariculture. For example, the DEPOMOD deposition model (Cromey et al. 2002) is routinely used by the Scottish regulatory agency, SEPA, as a tool for the sustainable management of salmon farming in Scottish sea lochs [SEPA (2008) Scottish Environment Protection Agency. <http://www.sepa.org.uk>. Cited 20 March]. This model was successfully adapted for predicting the deposition and benthic impacts produced by Mediterranean seabream and seabass cage aquaculture, and validated for the eastern Mediterranean in the framework of the MERAMED FP5 project (Meramed 2008, <http://meramed.akvaplan.com>). A second deposition model, the KK3D (Jusup et al. 2007), was recently applied for assessing the impact of a seabream and seabass fish farm in the Adriatic Sea. The results obtained from these works suggest the potential applicability of deposition models for routine seabream farm environmental impact assessment (EIA), currently lacking in Italy. The key input data for this class of models are the fluxes of wasted food and fish faeces released by the fish farm. These fluxes can be estimated from the field data for already existing farms, or via a detailed fish growth model. In fact, the second alternative allows one to simulate the impact of a fish farm and compare different management scenarios. A similar approach was implemented for carrying-capacity EIA studies in fjordic systems, in the MOM model (Ervik et al. 1997; Hansen et al. 2001; Stigebrandt et al. 2004), to adjust the local environmental impact of fish farming to the holding capacity of the site. The associated MOM modelling system [MOM (2008) The MOM website. <http://www.ancylus.net>. Cited 20 March] is an advanced tool in the field of aquaculture numerical modelling; see Stigebrandt et al. (2004). The model suite includes: (1) a growth module, (2) a dispersion module that computes the distribution of particulate matter from the net pens on the bottom for various sizes of pens and distances between them, (3) a benthic sub-model, which computes the maximum rate of particulate matter sedimentation which will prevent the extinction of the benthic macrofauna. However, the MOM-integrated system has not yet been validated for the Mediterranean environment and does not include a growth model for *S. aurata*.

To date, different models have been developed for predicting the growth of *S. aurata* in response to varying conditions of environmental forcing. Within the recent literature, the most significant works were published by Lupatsch et al. (2003) and Hernández et al. (2003). The first work, which is based on a detailed nutritional approach, is focused on the optimisation of feeding regimes and the minimisation of aquaculture waste. The growth model proposed by these authors was identified under a restricted interval of temperature, ranging from 20 to 28°C, and, therefore, their results cannot be directly transferred to the simulation of growth in Mediterranean waters, where temperature ranges from 8 to 28°C. The model proposed by Hernández et al. (2003) was specifically designed to simulate the response of the growth rate to the seasonal variations in water temperature. However, this model is of little use for EIA, since it does not include the computation of the faeces production rate and composition as a function of feed composition. In fact, from an EIA perspective, a desirable property of a growth model, would be a detailed description of food utilisation in response to different diet compositions (e.g., Stigebrandt 1999).

In this work we present a growth model for *S. aurata*, which simulates the response of seabream growth rate to both temperature and diet composition. The model was identified on the basis of a set of species-specific physiological studies and then calibrated and validated by using a comprehensive set of biometric data collected in the Adriatic and Tyrrhenian Seas. It was then used to compare the daily and yearly budgets of waste feed and faeces from two cages located in the Adriatic and Tyrrhenian Seas respectively. A potential use of this model might be to provide the input for a deposition model (e.g., MERAMOD, KK3D) for the assessment of the impact of a seabream fish farm. The work was carried out in the framework of EU project no. 006540 [ECASA (2008) Ecosystem Approach to Sustainable Aquaculture, FP6 EU-funded project. <http://www.ecasa.org.uk>. Cited 20 March], focussed on the development and testing of numerical models for aquaculture site-selection and monitoring.

Methods

Growth model equations

The mathematical description of the growth of *S. aurata* as a function of body size, food ratio and temperature is based on an energy budget:

$$\frac{dw}{dt} = \frac{(A - C)}{\varepsilon_T}, \quad (1)$$

where w is the wet weight of the fish. The term A (J day^{-1}) is called the “net anabolism” and represents the net energy income through feeding, while the term C (J day^{-1}), which quantifies the energy losses of a starving individual, is called the “fasting catabolism”. In Eq. 1, the energy balance between A and C is converted into a mass balance by means of the ε_T parameter, which quantifies the average energy content of 1 g of somatic tissue and is a function of the wet weight of the fish.

The complete set of Eqs. 2–7, which specify the energy balance, is listed in Table 1. The energy income is the result of the ingestion and absorption processes. The ingestion rate, I , is proportional to the size of the gut, which, in turn, is taken as proportional to w^m , and to the function $H(T_w)$, which takes into account the dependence of the ingestion on the water temperature. In our model, the ingestion rate I is limited by the upper threshold I_{ration} , which varies with time, and represents the amount of food available computed on the basis of the data on food quantity and number of individuals present in the cage; see Eq. 3. When these data are not available, as in the case of preliminary EIA, we assume that there is no food limitation, and therefore the I_{ration} is always equal to I .

According to the experimental evidence reported by Requena et al. (1997), proteins, carbohydrates and lipids have different levels of digestibility. Stigebrandt (1999) claimed that these differences among digestibility are of key importance for correctly predicting the impact of the fish farm, since the release of ammonium and phosphate is proportional to the feed protein content. This was taken into account in Eq. 4a, where the parameters β_p , β_C and β_L represent, respectively, the fraction of proteins, carbohydrates and lipids in fish food that can actually be assimilated. The digestibility parameters are used in Eq. 4b, for specifically computing the individual faecal production rate, F , based on the approach proposed by Stigebrandt (1999). The α parameter, in Eq. 4a, quantifies the energy costs regarding the digestion, assimilation, transportation and biochemical treatment of food. These energy losses are considered to be in proportion to the assimilated food.

Table 1 Functional expressions used in the *S. aurata* growth model

1. Functional expressions for net anabolism	Eq. no.
$I = I_{\max} \cdot H(T_w) \cdot w^m$	2
$\begin{cases} I = I_{\text{ration}}, & \text{when } I \geq I_{\text{ration}} \\ I = 0, & \text{when } T < 12^\circ\text{C} \end{cases}$	3
$A = (1 - \alpha) \cdot I \cdot [C_P \cdot \varepsilon_P \cdot \beta_P + C_C \cdot \varepsilon_C \cdot \beta_C + C_L \cdot \varepsilon_L \cdot \beta_L]$	4a
$F = I \cdot [C_P \cdot (1 - \beta_P) + C_C \cdot (1 - \beta_C) + C_L \cdot (1 - \beta_L)]$	4b
2. Functional expressions for fasting catabolism	Eq. no.
$C = \varepsilon_{O_2} \cdot k_0 \cdot K(T_w) \cdot w^n$	5
$H(T_w) = \left(\frac{T_m - T_w}{T_m - T_o} \right)^{b \cdot (T_m - T_o)} \cdot e^{b \cdot (T_w - T_o)}$	6
$K(T_w) = e^{pk \cdot T_w}$	7

State variable: w , fresh weight (g)

Forcings: T_w , water temperature ($^\circ\text{C}$); I_{ration} , amount of food provided by the farmer per gram of individual day^{-1} ; C_P , % of proteins in the ingested food; C_C , % of carbohydrates in the ingested food; C_L , % of lipids in the ingested food

Parameters: I_{\max} , maximum ingestion rate (day^{-1}); α feeding catabolism coefficient; β_P , assimilation coefficient for protein; β_C , assimilation coefficient for carbohydrate; β_L , assimilation coefficient for lipid; ε_P , energy content of protein (kJ g^{-1}); ε_C , energy content of carbohydrate (kJ g^{-1}); ε_L , energy content of lipid (kJ g^{-1}); ε_{O_2} , energy consumed by the respiration of 1 g of oxygen (kJ g^{-1}); ε_T , energy content of somatic tissue (kJ g^{-1}); pk , temperature coefficient for the fasting catabolism ($^\circ\text{C}^{-1}$); k_0 , fasting catabolism at 0°C (day^{-1}); m , weight exponent for the anabolism; n , weight exponent for the catabolism; b , shape coefficient for the $H(T_w)$ function; T_o , optimal temperature for *S. aurata* ($^\circ\text{C}$); T_m , maximum lethal temperature for *S. aurata* ($^\circ\text{C}$)

The term C , Eq. 5, quantifies the loss of energy due to the maintenance of living functions of a fasting fish. It is called “fasting catabolism”, and it depends on the size of the fish and on the temperature. Both the anabolic and catabolic processes are strongly affected by water temperature, T_w , because they are mediated by enzymatic kinetics. The relation between the rate of ingestion and the water temperature was described by using the general function proposed by Solidoro et al. (2000), see Eq. 6, which is defined between 0 and T_m , reaches a maximum in correspondence of T_o and then decreases. As regards the catabolic function $K(T_w)$, Eq. 7, we assumed a simple exponential dependence, in accordance with the literature (Jorgensen 1976; Cacho 1990).

Growth model parameters

The quantitative description of seabream growth requires the specification of 16 parameters, which were estimated on the basis of the specific literature and field observations:

1. The subset of parameters that specifies the net anabolism was fixed on the basis of the literature references;
2. The r_0 and pk fasting catabolism parameters were estimated on the basis of the oxygen consumption measurements taken from Guinea and Fernandez (1997);
3. The b parameter which defines the shape of the anabolic temperature function, was calibrated by fitting the model to the unpublished field data collected at Porto Ercole.

The model parameters, are listed in Table 2 together with their sources. As regards the parameters at point 1, the I_{\max} parameter which defines the ingestion rate at the optimal temperature, is the average between the ingestion rates reported by Robaina et al. (1995) and Santinha et al. (1999). The m coefficient which determines the dependence of the ingestion rate on the weight of the individual, was fixed to 0.6, in accordance with the value estimated by Lupatsch et al. (2003). The work by Requena et al. (1997) treats the effects of temperature on the energy budget of *S. aurata*. This study presents a measure of the specific dynamic action (SDA), which is the difference between the daily average oxygen consumption rate and the resting oxygen consumption rate. The SDA was found to be approximately 30% of the absorbed energy: this ratio represents the value for the feeding anabolism coefficient, α , used in the model. According to Requena et al. (1997), the protein digestibility is about 85% and for lipids is 95%. Carbohydrates digestibility was fixed at 63%, according to the values measured by Lupatsch et al. (1997). The energy contents for the proteins, lipids and carbohydrates were measured by Brett and Groves (1979), while the energy loss associated with the respiration of 1 g of oxygen was quantified by Brafield and Solomon (1972). The energy content of the fish tissues, ε_T , is a nonlinear function of the wet body weight, taking into account the different lipid/protein ratio, which characterises fishes of different sizes. The function used in the model to define the ε_T was estimated using data from Lupatsch et al. (2003), by fitting the tissue energy content of 35 individuals weighing between 20 and 450 g. The optimal temperature and

Table 2 Parameters used in the *S. aurata* growth model and their sources

Parameter	Description	Value	Unit	Source
I_{\max}	Maximum ingestion rate	0.09	day ⁻¹	Robaina et al. (1995) and Santinha et al. (1999)
α	Feeding catabolism coefficient	0.3	–	Requena et al. (1997)
β_P	Assimilation coefficient for protein	0.85	–	Requena et al. (1997)
β_C	Assimilation coefficient for carbohydrate	0.5	–	Stigebrandt (1999)
β_L	Assimilation coefficient for lipid	0.95	–	Requena et al. (1997)
ε_P	Energy content of protein	23.6	kJ g ⁻¹	Brett and Groves (1979)
ε_C	Energy content of carbohydrate	17.2	kJ g ⁻¹	Brett and Groves (1979)
ε_L	Energy content of lipid	36.2	kJ g ⁻¹	Brett and Groves (1979)
ε_{O_2}	Energy consumed by the respiration of 1 g of oxygen	13.6	kJ g ⁻¹	Brafield and Solomon (1972)
ε_T	Energy content of somatic tissue	4.66 w ^{0.14}	kJ g ⁻¹	Lupatsch et al. (2003)
pk	Temperature coefficient for the fasting catabolism	0.06	°C ⁻¹	Estimated from Guinea and Fernandez (1997)
k_0	Fasting catabolism at 0°C	0.00072	day ⁻¹	Estimated from Guinea and Fernandez (1997)
m	Weight exponent for the anabolism	0.6	–	Lupatsch et al. (2003)
n	Weight exponent for the catabolism	1.0	–	
b	Shape coefficient for the $H(T_w)$ function	0.2	–	Model calibration
T_o	Optimal temperature for <i>S. aurata</i>	25	°C	Ravagnan (1984)
T_m	Maximum lethal temperature for <i>S. aurata</i>	32.9	°C	Hernández et al. (2003)

maximum lethal temperatures, T_o and T_m , were taken to be equal to those specified by Hernández et al. (2003), who used a function similar to Eq. 5 to model the growth of the gilthead seabream in water temperatures ranging between 3 and 32.9°C. In keeping with the observations made by Ravagnan (1995), a lower feeding threshold of 12°C was considered, below which the fish has no appetite.

The estimations of the r_0 and p_k are based on a set of oxygen consumption data reported in Guinea and Fernandez (1997), who studied the response of the seabream metabolism to water temperature variations. As we were seeking an estimate of the fasting catabolism, we took into consideration the minimum rate of oxygen consumption at a given temperature. The values for r_0 and p_k reported in Table 2, were obtained by fitting the oxygen consumption rates measured at 16, 21 and 24°C by means of the following equation:

$$\frac{dO_2}{dt} = k_0 \cdot e^{(p_k \cdot T_w)} \cdot w^n \quad (8)$$

Model calibration

The b parameter, which defines the shape of the temperature function used in the $H(T_w)$ anabolic term was calibrated by comparing the model output with a time series of field data. The remaining 16 parameters were fixed on the basis of several species-specific physiological studies. The decision to calibrate a single parameter was aimed at increasing the robustness of the estimation. The model calibration was carried out by minimising the goal function,

$$\Gamma = \sum_{i=1}^n (W_i - \hat{W}_i)^2, \quad (9)$$

where W_i and \hat{W}_i represent the observed and predicted wet weight of the fish respectively.

The minimum of Γ was searched by means of a simplex algorithm (Press et al. 1987). The ordinary differential equation describing the growth, Eq. 1, was numerically solved by using a fourth-order Runge-Kutta scheme (Press et al. 1987).

Field data

The individual-based growth model was calibrated and validated using a set of water temperature and husbandry data collected in the Tyrrhenian and Adriatic Seas respectively; see Fig. 1. The first dataset was collected at a fish farm located 2,500 m east of Porto Ercole (Tuscany, Italy); it includes monthly data concerning the total biomass and number of individuals in a single cage together with the water temperature measurements. The time series covers one rearing cycle, starting in July 2001 and ending in June 2002. The second dataset was collected at the Co. Pro. Mar. fish farm in Bisceglie (Puglia, Italy). Data from six different cages, concerning the years 2004 and 2005, were made available, combined with the monthly water temperature in the area. In this case, the growth data include the total number and average wet weight of the individuals at both seedling and harvesting times. At this site, the biometric data were determined toward the end of the rearing cycle. In both cases, i.e. Porto Ercole and Bisceglie, the farmer provided monthly data on the composition and quantity of feed used. For more detailed data about the Porto Ercole fish farm, see Porrello et al. (2005).

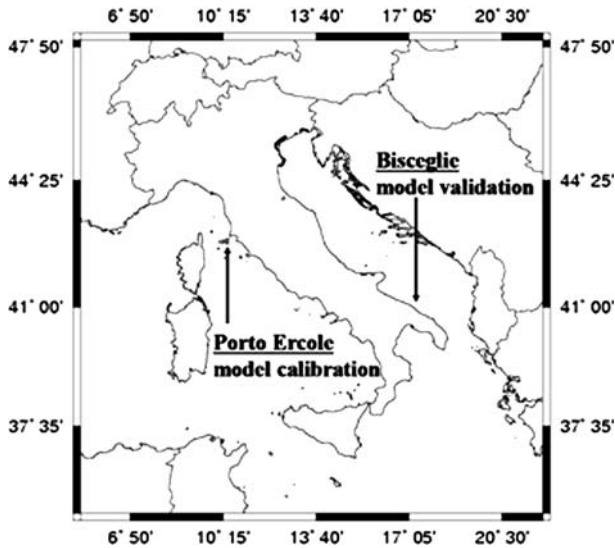


Fig. 1 Location of the two sites at which field data for model calibration and validation were collected

Results

Model calibration

Parameter b (see Eq. 6) was estimated by calibrating the model on the wet weight data measured in Porto Ercole. The model output is compared with the observations in Fig. 2: the wet weight of the individual predicted by the model is in good agreement with the field observations, with an R^2 of 0.99. The value of b , which minimises the goal function Γ , is 0.2. The resulting Q_{10} for the net anabolism, computed as the ratio between $H(T_w)$ at 25 and 15°C, is 2.03.

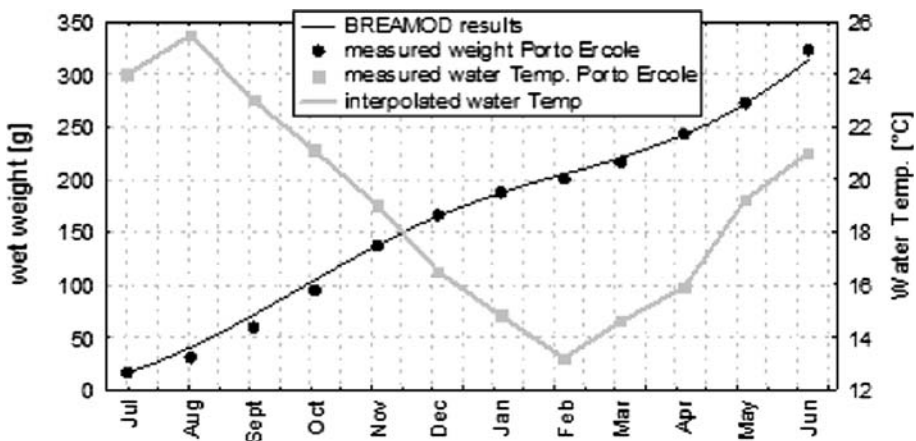


Fig. 2 Calibration of the seabream growth model

Model validation

The validation of the individual-based growth model was carried out by using a dataset including the water temperature, fish wet weight, number of individuals and feeding regime, collected from six different cages located off-shore from the town of Bisceglie, in the southern Adriatic Sea. In this case, the growth was not monitored as regularly as in Porto Ercole: in fact, only initial weights and those measured at the end of the rearing cycle were recorded. The individual-based model was run independently at each cage, using as initial condition the wet weight at the beginning of the rearing cycle. The time series of water temperatures used to force the model is reported in Fig. 3. As can be seen there, the Bisceglie site is characterised by lower winter temperatures than Porto Ercole. In particular, in the coldest months, fish stop feeding, since the water temperature drops below the set threshold. The model growth curves and the field data concerning the six cages studied in Bisceglie are reported in Fig. 4. As can be seen, at cage 1, model predictions are in good accordance with field data, while at cages 2, 5 and 19, the model underestimates, and at cages 6 and 21, it slightly overestimates the observed weights. In the case of cage 19, model fit was evaluated on a set of only two observed weights. In general, these results seem to indicate that the model reasonably predicts the growth of the individual when forced using a set of environmental data different from that used in the calibration.

Model predicted excretion rates

Figure 5a, b shows a comparison between the model predicted rate of excretion, with regard to a fish reared at the Bisceglie site, in cage 1, and at Porto Ercole. These estimations are based on site-specific data on food composition, which differed slightly between the two sites; see Table 3. The maximum rates of excretion for the three compounds are comparable at the two sites; the rate of carbohydrate excretion is lower in Porto Ercole, where the food has a higher protein content. As regards the Bisceglie site, the model predicts a stop in fish excretion, which corresponded with the time window during which the water temperature drops below the threshold of 12°C.

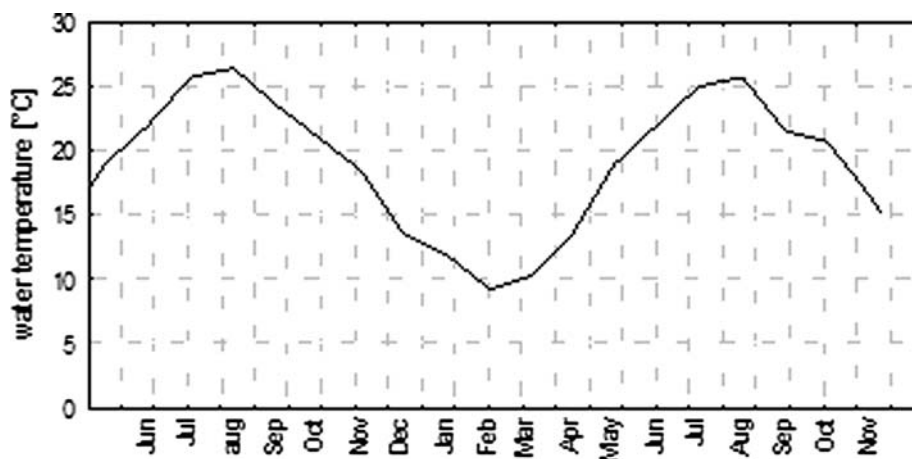


Fig. 3 Water temperature at the validation site (Bisceglie)

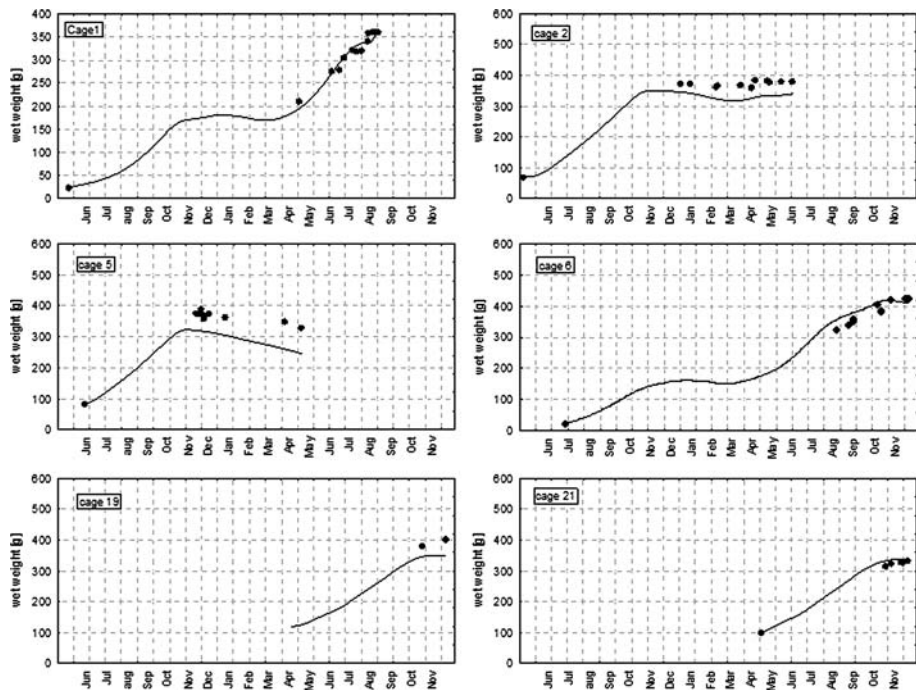


Fig. 4 Validation of the seabream growth model: growth trajectories predicted by the model (*continuous lines*) are compared with the field data (*points*) collected in Bisceglie

Discussion

Modelling the growth response to water temperature

The shape of the $H(T_w)$ function (Eq. 6) used to describe the response of fish anabolism to water temperature depends on parameter b , which was calibrated by fitting the model to the Porto Ercole field data. The curve obtained is compared in Fig. 6 with the one proposed by Hernández et al. (2003). The two curves present a similar behaviour, reaching a maximum at a temperature of 25°C, and are both defined in the range between 0 and 32.9°C (the upper lethal temperature for this species). The Q_{10} computed for the Hernández et al. (2003) formulation, between 15 and 25°C, is about 1.68, which is lower than, but comparable to our value of 2.03. The advantages of using Eq. 6 with respect to the Hernández et al. (2003) model are the following:

- The response to the water temperature is simulated by using three parameters instead of five.
- The optimal temperature is defined explicitly by using a parameter that has a physiological meaning.
- The function varies between 0 and 1.

Comparison between husbandry practices at the two sites

The amount of food supplied at cage 5, in Bisceglie, is shown in Fig. 7. This profile was obtained by using the feeding tables and the data on fish abundance provided by the

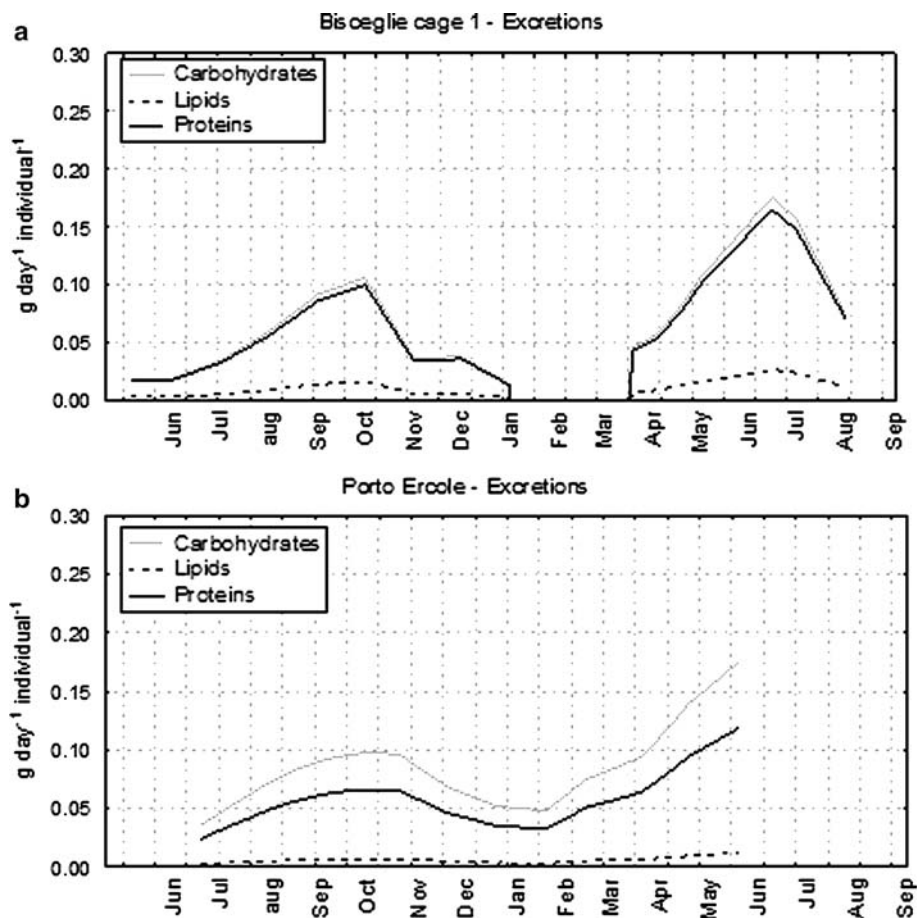


Fig. 5 **a, b** Rate of excretion of carbohydrates, proteins and lipids as computed by the model on the basis of food composition data and digestibility coefficients. **a** Bisceglie cage 1; **b** Porto Ercole

Table 3 Food composition at Bisceglie and Porto Ercole sites

	Bisceglie (%)	Porto Ercole (%)
Protein content	44	51
Lipid content	21	17
Carbohydrate content	19	14

farmers. An interesting feature of the model, when used in combination with the food data provided by the farmer, is the possibility of taking into account food scarcity and estimating food wastage. As one can see in Fig. 7, there was no food supplied to cage 5 from February onwards. This led to the weight decrease predicted by the model at cage 5, and was also corroborated by the field data (see Fig. 4). On the other hand, by comparing the food supplied by the farmer with the fish ingestion rate predicted by the model, one can obtain useful indications on the amount of uneaten feed, which is wasted. As shown in

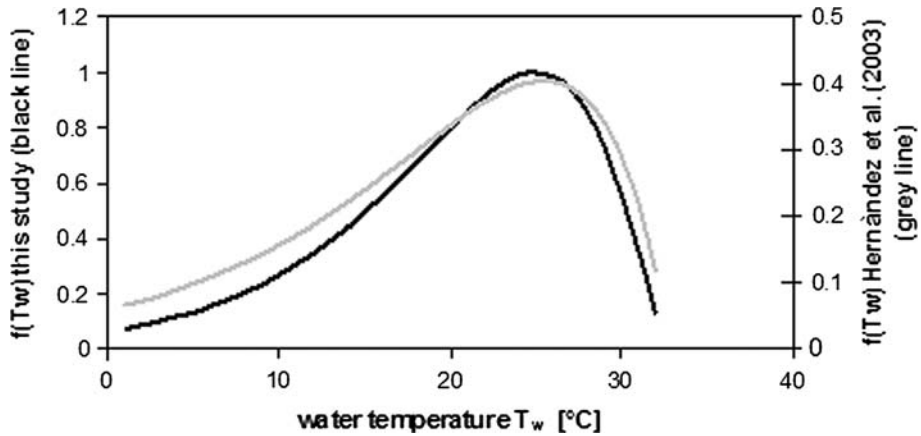


Fig. 6 Comparison between the water temperature function used in this study and the formulation used by Hernández et al. (2003)

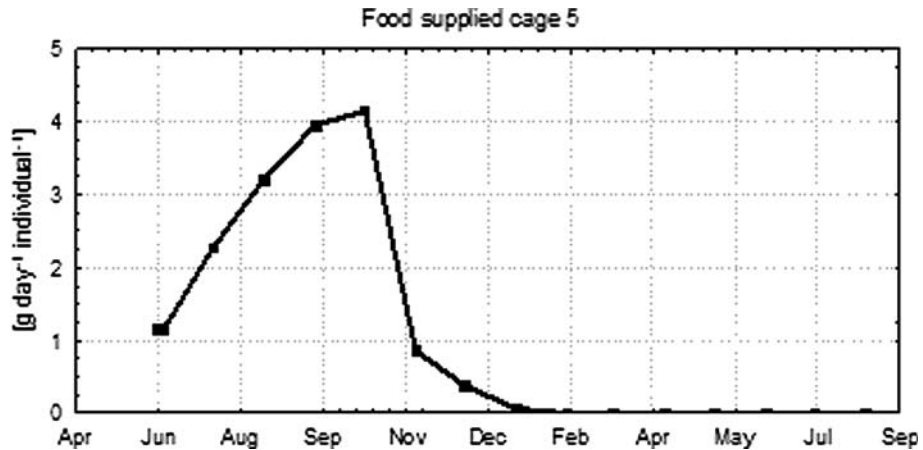


Fig. 7 Amount of food available per individual at the Bisceglie site, cage 5. The time series were computed from the feeding tables provided by the fish farmers

Fig. 8, during the winter period both the food supplied by the farmer and the model-predicted ingestion rate are at very low values, reaching 0 in the time window in which the water temperature goes below 12°C. However, during the spring, the fish ingestion rate remains below the available food supply. The difference between these two quantities provides the food waste estimation reported in Fig. 9a. The same estimations performed at the Porto Ercole site, Fig. 9b, indicate that the amount of feed wasted per individual at this site is potentially lower. However, in the time window comprising November and March, the food available at this site goes below the model predicted ingestion rate, thus causing a decrease in the fish growth rate.

Starting from the individual rates predicted by the model and reported in Fig. 10a, b, one can estimate the overall mass budget for a cage by knowing the total number of reared individuals. The number of individuals contained in the cage, N , can be calculated according to the equation,

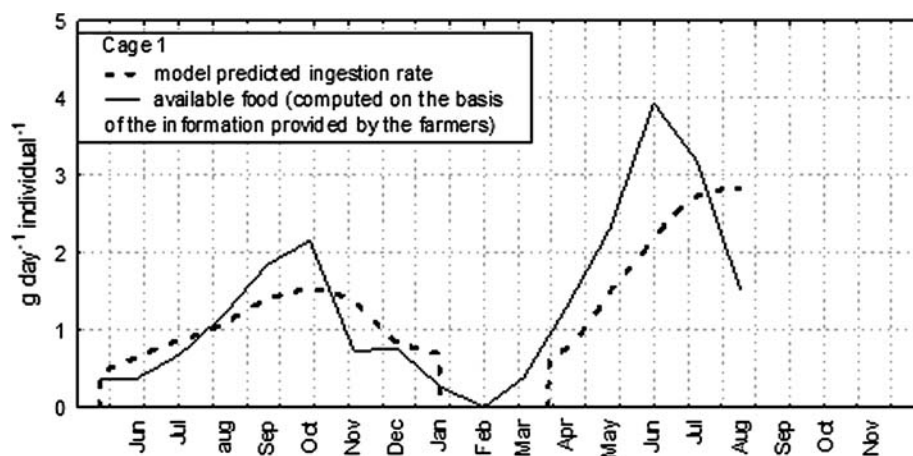


Fig. 8 Model predicted ingestion rate and available food per individual at cage 1 (Bisceglie)

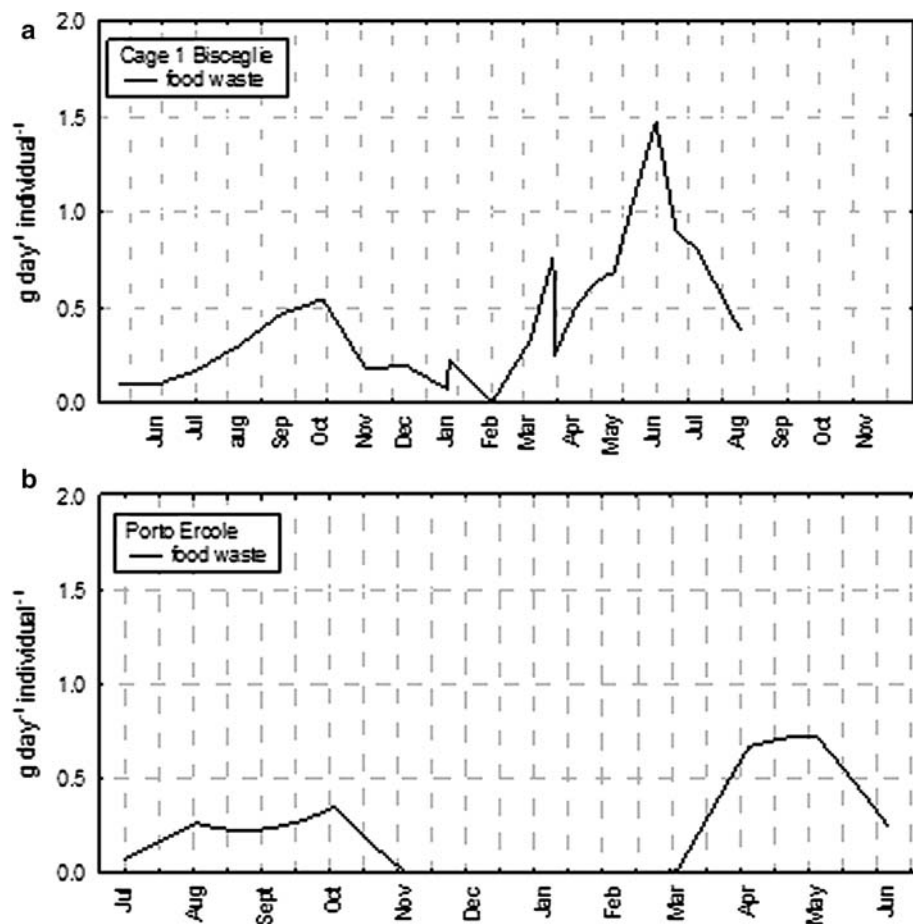


Fig. 9 a, b Predicted waste of food at Bisceglie, cage 1, and Porto Ercole sites

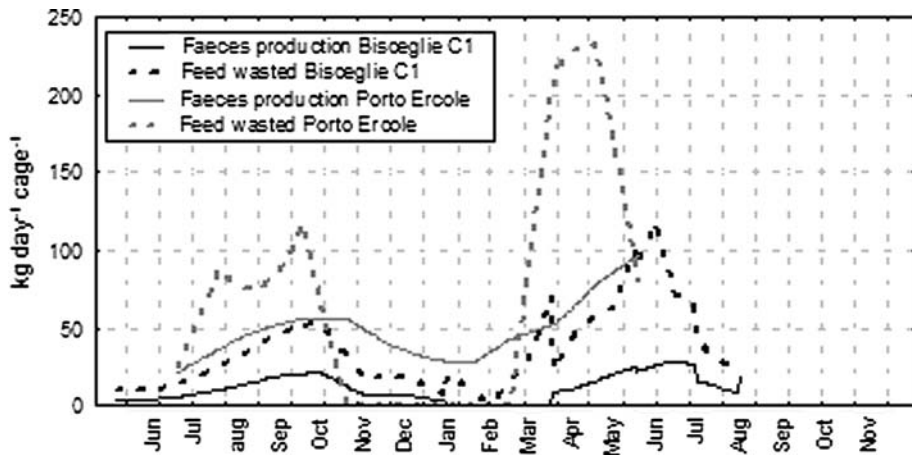


Fig. 10 Total rate of food and faeces production predicted by the model at Bisceglie cage 1 (black) and Porto Ercole (grey)

$$\frac{dN}{dt} = -m \cdot N - h, \quad (10)$$

where t is time, m is the natural mortality rate, which is assumed to be constant in time, and h is the harvesting rate. The time series of feed wasted and faeces produced at the two cages located, respectively, in Bisceglie and Porto Ercole are reported in Fig. 10. As regards the Bisceglie site, coloured in black, we estimated that there was a total food wastage of 16.2×10^3 kg, integrated over the whole rearing cycle, with an average wastage rate of $35 \text{ kg cage}^{-1} \text{ day}^{-1}$. The total faeces production is of 5.4×10^3 kg, with an average production rate of $11 \text{ kg cage}^{-1} \text{ day}^{-1}$. These predictions are in good agreement with the ones derived from a preliminary application of the MOM model at the Bisceglie study site at cage 1 (Stigtebrandt, personal communication). The flux of particulate matter computed by MOM per 10^3 kg of fish production is 163 kg of faeces and 563 kg of wasted food. These values, when multiplied by the total cage production along one rearing cycle, 29×10^3 kg, give a total food wastage of 16.3×10^3 kg, and a faeces wastage of 4.7×10^3 kg, with the values respectively representing 30% and 9% of the total food provided by the farmer at this cage (54.4×10^3 kg).

The Porto Ercole site, coloured grey in Fig. 10, was characterised by a higher fish density, on average 3.5 times that of the Bisceglie, and a faster rearing cycle, 12 instead of 15 months. For this reason, the Porto Ercole cage presents a higher wastage of feed and faeces, respectively, of 23.9×10^3 and 16.3×10^3 kg over the whole rearing cycle, even though the model budgets computed for a single individual indicated that the food wastage at this site is potentially lower compared to that at Bisceglie (Fig. 9a, b).

Conclusions

In this work, an individual-based growth model for the gilthead seabream *S. aurata* was developed and applied by using original field data collected in the Adriatic and Tyrrhenian Seas. The validation performed indicates that the model behaves reasonably for water

temperatures between 9 and 26°C. The detailed description of the food utilisation in response to the different diet compositions allowed us to compute the mass budget of uneaten food and faeces produced by a fish cage, and to compare the husbandry practices at two Italian fish farms. From an applied perspective, the future use of this growth model in relation to mariculture might typically be to estimate the amounts of uneaten food and faeces arising from the farm, thus providing an input for a deposition model (e.g., MERAMOD, KK3D). The integration of growth and deposition models into a single system, using an approach similar to the one adopted in Norway with the MOM model, could provide a useful tool for the site-selection and monitoring of finfish mariculture operations in Mediterranean environments.

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